

OIPE

#2

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/930,125

TIME: 17:22:05

Input Set : A:\544.app.txt

Output Set: N:\CRF3\08162001\I930125.raw

ENTERED

C-->

4 <110> APPLICANT: Hand-Zimmerman, Susan
 5 Cheever, Martin A.
 6 Foy, Teresa M.
 7 Lodes, Michael J.
 8 Kalos, Michael D.
 9 McNeill, Patricia D.
 10 Vedvick, Thomas S.
 13 <120> TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS
 14 OF HER-2/NEU-ASSOCIATED MALIGNANCIES
 17 <130> FILE REFERENCE: 210121.544
 19 <140> CURRENT APPLICATION NUMBER: US/09/930,125
 20 <141> CURRENT FILING DATE: 2001-08-14
 22 <160> NUMBER OF SEQ ID NOS: 25
 24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 3768
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapien
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)...(3765)
 35 <400> SEQUENCE: 1
 36 atg gag ctg gcg gcc ttg tgc cgc tgg ggg ctc ctc ctc gcc ctc ttg 48
 37 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 38 1 5 10 15
 40 ccc ccc gga gcc gcg agc acc caa gtg tgc acc ggc aca gac atg aag 96
 41 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
 42 20 25 30
 44 ctg cgg ctc cct gcc agt ccc gag acc cac ctg gac atg ctc cgc cac 144
 45 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
 46 35 40 45
 48 ctc tac cag ggc tgc cag gtg gtg cag gga aac ctg gaa ctc acc tac 192
 49 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
 50 50 55 60
 52 ctg ccc acc aat gcc agc ctg tcc ttc ctg cag gat atc cag gag gtg 240
 53 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
 54 65 70 75 80
 56 cag ggc tac gtg ctc atc gct cac aac caa gtg agg cag gtc cca ctg 288
 57 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
 58 85 90 95
 60 cag agg ctg cgg att gtg cga ggc acc cag ctc ttt gag gac aac tat 336
 61 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
 62 100 105 110
 64 gcc ctg gcc gtg cta gac aat gga gac ccg ctg aac aat acc acc cct 384
 65 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
 66 115 120 125
 68 gtc aca ggg gcc tcc cca gga ggc ctg cgg gag ctg cag ctt cga agc 432

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69	Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser	
70	130 135 140	
72	ctc aca gag atc ttg aaa gga ggg gtc ttg atc cag cgg aac ccc cag	480
73	Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln	
74	145 150 155 160	
76	ctc tgc tac cag gac acg att ttg tgg aag gac atc ttc cac aag aac	528
77	Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn	
78	165 170 175	
80	aac cag ctg gct ctc aca ctg ata gac acc aac cgc tct cgg gcc tgc	576
81	Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys	
82	180 185 190	
84	cac ccc tgt tct ccg atg tgt aag ggc tcc cgc tgc tgg gga gag agt	624
85	His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser	
86	195 200 205	
88	tct gag gat tgt cag agc ctg acg cgc act gtc tgt gcc ggt ggc tgt	672
89	Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys	
90	210 215 220	
92	gcc cgc tgc aag ggg cca ctg ccc act gac tgc tgc cat gag cag tgt	720
93	Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys	
94	225 230 235 240	
96	gct gcc ggc tgc acg ggc ccc aag cac tct gac tgc ctg gcc tgc ctc	768
97	Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu	
98	245 250 255	
100	cac ttc aac cac agt ggc atc tgt gag ctg cac tgc cca gcc ctg gtc	816
101	His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val	
102	260 265 270	
104	acc tac aac aca gac acg ttt gag tcc atg ccc aat ccc gag ggc cgg	864
105	Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg	
106	275 280 285	
108	tat aca ttc ggc gcc agc tgt gtg act gcc tgt ccc tac aac tac ctt	912
109	Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu	
110	290 295 300	
112	tct acg gac gtg gga tcc tgc acc ctc gtc tgc ccc ctg cac aac caa	960
113	Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln	
114	305 310 315 320	
116	gag gtg aca gca gag gat gga aca cag cgg tgt gag aag tgc agc aag	1008
117	Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys	
118	325 330 335	
120	ccc tgt gcc cga gtg tgc tat ggt ctg ggc atg gag cac ttg cga gag	1056
121	Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu	
122	340 345 350	
124	gtg agg gca gtt acc agt gcc aat atc cag gag ttt gct ggc tgc aag	1104
125	Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys	
126	355 360 365	
128	aag atc ttt ggg agc ctg gca ttt ctg ccg gag agc ttt gat ggg gac	1152
129	Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp	
130	370 375 380	
132	cca gcc tcc aac act gcc ccg ctc cag cca gag cag ctc caa gtg ttt	1200
133	Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe	

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134	385	390	395	400	
136	gag act ctg gaa gag atc aca ggt tac cta tac atc tca gca tgg ccg	1248			
137	Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro				
138		405	410	415	
140	gac agc ctg cct gac ctc agc gtc ttc cag aac ctg caa gta atc cgg	1296			
141	Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg				
142		420	425	430	
144	gga cga att ctg cac aat ggc gcc tac tcg ctg acc ctg caa ggg ctg	1344			
145	Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu				
146		435	440	445	
148	ggc atc agc tgg ctg ggg ctg cgc tca ctg agg gaa ctg ggc agt gga	1392			
149	Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly				
150		450	455	460	
152	ctg gcc ctc atc cac cat aac acc cac ctc tgc ttc gtg cac acg gtg	1440			
153	Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val				
154		465	470	475	480
156	ccc tgg gac cag ctc ttt cgg aac ccg cac caa gct ctg ctc cac act	1488			
157	Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr				
158		485	490	495	
160	gcc aac cgg cca gag gac gag tgt gtg ggc gag ggc ctg gcc tgc cac	1536			
161	Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His				
162		500	505	510	
164	cag ctg tgc gcc cga ggg cac tgc tgg ggt cca ggg ccc acc cag tgt	1584			
165	Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys				
166		515	520	525	
168	gtc aac tgc agc cag ttc ctt cgg ggc cag gag tgc gtg gag gaa tgc	1632			
169	Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys				
170		530	535	540	
172	cga gta ctg cag ggg ctc ccc agg gag tat gtg aat gcc agg cac tgt	1680			
173	Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys				
174		545	550	555	560
176	ttg ccg tgc cac cct gag tgt cag ccc cag aat ggc tca gtg acc tgt	1728			
177	Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys				
178		565	570	575	
180	ttt gga ccg gag gct gac cag tgt gtg gcc tgt gcc cac tat aag gac	1776			
181	Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp				
182		580	585	590	
184	cct ccc ttc tgc gtg gcc cgc tgc ccc agc ggt gtg aaa cct gac ctc	1824			
185	Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu				
186		595	600	605	
188	tcc tac atg ccc atc tgg aag ttt cca gat gag gag ggc gca tgc cag	1872			
189	Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln				
190		610	615	620	
192	cct tgc ccc atc aac tgc acc cac tcc tgt gtg gac ctg gat gac aag	1920			
193	Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys				
194		625	630	635	640
196	ggc tgc ccc gcc gag cag aga gcc agc cct ctg acg tcc atc atc tct	1968			
197	Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser				
198		645	650	655	

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200	gcg gtg gtt ggc att ctg ctg gtc gtg gtc ttg ggg gtg gtc ttt ggg	2016
201	Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly	
202	660	
204	atc ctc atc aag cga cgg cag cag aag atc cgg aag tac acg atg cgg	2064
205	Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg	
206	675	
208	aga ctg ctg cag gaa acg gag ctg gtg gag ccg ctg aca cct agc gga	2112
209	Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly	
210	690	
212	gcg atg ccc aac cag gcg cag atg cgg atc ctg aaa gag acg gag ctg	2160
213	Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu	
214	705	
216	agg aag gtg aag gtg ctt gga tct ggc gct ttt ggc aca gtc tac aag	2208
217	Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys	
218	725	
220	ggc atc tgg atc cct gat ggg gag aat gtg aaa att cca gtg gcc atc	2256
221	Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile	
222	740	
224	aaa gtg ttg agg gaa aac aca tcc ccc aaa gcc aac aaa gaa atc tta	2304
225	Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu	
226	755	
228	gac gaa gca tac gtg atg gct ggt gtg ggc tcc cca tat gtc tcc cgc	2352
229	Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg	
230	770	
232	ctt ctg ggc atc tgc ctg aca tcc acg gtg cag ctg gtg aca cag ctt	2400
233	Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu	
234	785	
236	atg ccc tat ggc tgc ctc tta gac cat gtc cgg gaa aac cgc gga cgc	2448
237	Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg	
238	805	
240	ctg ggc tcc cag gac ctg ctg aac tgg tgt atg cag att gcc aag ggg	2496
241	Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly	
242	820	
244	atg agc tac ctg gag gat gtg cgg ctc gta cac agg gac ttg gcc gct	2544
245	Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala	
246	835	
248	cgg aac gtg ctg gtc aag agt ccc aac cat gtc aaa att aca gac ttc	2592
249	Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe	
250	850	
252	ggg ctg gct cgg ctg ctg gac att gac gag aca gag tac cat gca gat	2640
253	Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp	
254	865	
256	ggg ggc aag gtg ccc atc aag tgg atg gcg ctg gag tcc att ctc cgc	2688
257	Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg	
258	885	
260	cgg cgg ttc acc cac cag agt gat gtg tgg agt tat ggt gtg act gtg	2736
261	Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val	
262	900	
264	tgg gag ctg atg act ttt ggg gcc aaa cct tac gat ggg atc cca gcc	2784

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265	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	
266			915					920					925				
268	cgg	gag	atc	cct	gac	ctg	ctg	gaa	aag	ggg	gag	cgg	ctg	ccc	cag	ccc	2832
269	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	
270		930					935					940					
272	ccc	atc	tgc	acc	att	gat	gtc	tac	atg	atc	atg	gtc	aaa	tgt	tgg	atg	2880
273	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met	
274	945				950					955					960		
276	att	gac	tct	gaa	tgt	cgg	cca	aga	ttc	cgg	gag	ttg	gtg	tct	gaa	ttc	2928
277	Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe	
278				965					970					975			
280	tcc	cgc	atg	gcc	agg	gac	ccc	cag	cgc	ttt	gtg	gtc	atc	cag	aat	gag	2976
281	Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu	
282			980					985					990				
284	gac	ttg	ggc	cca	gcc	agt	ccc	ttg	gac	agc	acc	ttc	tac	cgc	tca	ctg	3024
285	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu	
286		995					1000					1005					
288	ctg	gag	gac	gat	gac	atg	ggg	gac	ctg	gtg	gat	gct	gag	gag	tat	ctg	3072
289	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu	
290	1010					1015				1020							
292	gta	ccc	cag	cag	ggc	ttc	ttc	tgt	cca	gac	cct	gcc	ccg	ggc	gct	ggg	3120
293	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly	
294	1025				1030				1035				1040				
296	ggc	atg	gtc	cac	cac	agg	cac	cgc	agc	tca	tct	acc	agg	agt	ggc	ggt	3168
297	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly	
298			1045					1050				1055					
300	ggg	gac	ctg	aca	cta	ggg	ctg	gag	ccc	tct	gaa	gag	gag	gcc	ccc	agg	3216
301	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg	
302		1060					1065				1070						
304	tct	cca	ctg	gca	ccc	tcc	gaa	ggg	gct	ggc	tcc	gat	gta	ttt	gat	ggt	3264
305	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	
306		1075				1080				1085							
308	gac	ctg	gga	atg	ggg	gca	gcc	aag	ggg	ctg	caa	agc	ctc	ccc	aca	cat	3312
309	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	Pro	Thr	His	
310	1090				1095					1100							
312	gac	ccc	agc	cct	cta	cag	cgg	tac	agt	gag	gac	ccc	aca	gta	ccc	ctg	3360
313	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu	
314	1105			1110				1115				1120					
316	ccc	tct	gag	act	gat	ggc	tac	gtt	gcc	ccc	ctg	acc	tgc	agc	ccc	cag	3408
317	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	
318		1125				1130					1135						
320	cct	gaa	tat	gtg	aac	cag	cca	gat	gtt	cgg	ccc	cag	ccc	cct	tcg	ccc	3456
321	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	
322		1140				1145					1150						
324	cga	gag	ggc	cct	ctg	cct	gct	gcc	cga	cct	gct	ggt	gcc	act	ctg	gaa	3504
325	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	
326		1155				1160					1165						
328	agg	ccc	aag	act	ctc	tcc	cca	ggg	aag	aat	ggg	gtc	gtc	aaa	gac	gtt	3552
329	Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp	Val	

VERIFICATION SUMMARY

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L:19 M:270 C: Current Application Number differs, Wrong Format

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